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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141; ]

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Reviewer Comments:

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147  
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291  
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
80 85 90

Please remove the blank line between the above row of codons and their respective amino acids; the amino acids should appear directly below their codons.

<210> 15  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1578)  
<223> k = g or t.

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1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu  
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe  
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195  
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala  
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243  
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr  
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly  
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339  
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro  
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
Val Gly Gly Cys Tyr Arg Leu Asp Ile Pro Met Ser Asn Cys Phe  
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr  
130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn  
145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531  
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu  
160 165 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579  
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe  
175 180 185 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cg <sup>g</sup> atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu				
210	215		220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala				
225	230		235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp				
240	245		250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat				819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp				
255	260		265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat				867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp				
275	280		285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc				915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe				
290	295		300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta				963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu				
305	310		315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt				1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser				
320	325		330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc				1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile				
335	340		345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag				1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys				
355	360		365	

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			
370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu			
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg			1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc			1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			
495	500	505	510
aac gat ggg tct gtc ata tagatcggt gcgtktgcg			1576
Asn Asp Gly Ser Val Ile			
515			

1) Please remove the blank line between the above row of codons and their amino acids; 2) the above <220>-<223> section describing "k" at

location 1578 is incorrect; the sequence only has 1576 nucleotides.  
Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and  
41.

<210> 33  
<211> 1576  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form, modified to be  
heat stable

<220>  
<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.

<220>  
<221> variation  
<222> (1008)  
<223> y = c or t.

<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.

<220>  
<221> variation  
<222> (1578)  
<223> k = g or t.

<400> 33  
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51  
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His  
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99  
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15	20	25	30
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt      147			
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe			
35	40	45	
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct      195			
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala			
50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat      243			
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr			
65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga      291			
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly			
80	85	90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct      339			
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro			
95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc      387			
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act      435			
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac      483			
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa      531			
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt      579			
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627  
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile  
195 200 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675  
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu  
210 215 220

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct 723  
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala  
225 230 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat 771  
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp  
240 245 250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat 819  
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp  
255 260 265 270

ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat 867  
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp  
275 280 285

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc 915  
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe  
290 295 300

aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta 963  
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu  
305 310 315

cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt 1011  
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser  
320 325 330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059  
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile  
335 340 345 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107  
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys

355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			1155
370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			1203
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			1251
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			1299
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Ala Ser Lys Leu			1347
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			1395
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtc gtc Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			1443
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			1491
480	485	490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			1539
495	500	505	510
aac gat ggg tct gtc ata tagatcggt gcgtktgcg Asn Asp Gly Ser Val Ile			1576
515			

Two errors above: 1) the <220>-<223> section describing the "y" at location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223> section describing the "k" at location 1578 is errored: there are only 1576 nucleotides above.

\*\*\*\*\*

Application No: 10569000

Version No: 2.0

### Input Set:

### **Output Set:**

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**Finished:** 2010-07-22 16:44:19.919  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 897 ms  
**Total Warnings:** 0  
**Total Errors:** 112  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

**Input Set:**

**Output Set:**

**Started:** 2010-07-22 16:44:17.022  
**Finished:** 2010-07-22 16:44:19.919  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 897 ms  
**Total Warnings:** 0  
**Total Errors:** 112  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.  
Hannah, L. Curtis  
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000  
<141> 2010-07-22

<150> US 60/496,188  
<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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<211> 1425  
<212> DNA  
<213> zea mays

<400> 1

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caacataacct caatcctcaa	
gctcatgata gtgttcttgg aatcattctg ggagggttgt	180
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ttgacaaaaga agcgtgccaa gcctgcagtgcattgggtg	240
ccaactatag actgattgat	
attcctgtca gcaattgtct caacagcaac atatccaaga	300
tctatgtgct aacgcaattt	
aactctgctt ccctcaaccg tacccctctca agagcctacg	360
ggagcaacat tggagggtac	
aagaatgaag ggtttggta agtcttagct gcacagcaga	420
gcccagataa tccaaactgg	
tttcaggta ctgcagatgc tgtaaggcag tacttggt	480
tgtttgagga gcataatgtg	
atggaatttc taattcttgc tggcgatcac ctgtaccgga	540
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caggcacaca gagaaacaaa tgctgatatt accgttgctg	600
ccctaccgat ggatgagaaa	
cgtgcaactg catttggcct catgaaaatt gatgaagaag	660
ggaggatcat tgagttgct	
gagaaaccca aaggagagca gttgaaagca atgatggtg	720
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gatgacgtga gggcaaagga aatgccttat attgctagca	780
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gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcataa aggtggaatt	1380
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 <211> 475  
 <212> PRT  
 <213> zea mays

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile			
35	40	45	

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys			
50	55	60	

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp			
65	70	75	80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val			
85	90	95	

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala			
100	105	110	

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val			
115	120	125	

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr			
130	135	140	

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val			
145	150	155	160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr			
165	170	175	

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val  
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met  
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys  
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu  
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe  
260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser  
275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp  
290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys  
305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr  
325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val  
340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile  
355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile  
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala  
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly  
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile  
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala  
435 440 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile  
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile  
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<210> 3  
<211> 1425  
<212> DNA  
<213> zea mays

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ttgacaaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatacg actgattgat 240  
attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtct aacgcaattt 300  
aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac 360  
aagaatgaag ggtttgttga agtcttagct gcacagcaga gcccagataa tccaaactgg 420  
tttcagggttta ctgcagatgc tgtaaggcag tacttgtgg tggtttagga gcataatgtg 480  
atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt 540  
cagggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa 600  
cgtgcaactg cattggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgc 660  
gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt 720  
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgtttcagc 780  
aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaaagt 840  
gaggttattc caggtgcaac cagcatttggaa aagagggttc aggcttatct gtatgtgg 900  
tactggaaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag 960  
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<211> 475

<212> PRT  
<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala  
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn  
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile  
35 40 45

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys  
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp  
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val  
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala  
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val  
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr  
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val  
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr  
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val  
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met  
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys  
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu  
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe  
                  260                 265                 270  
  
 Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser  
                  275                 280                 285  
  
 Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp  
                  290                 295                 300  
  
 Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys  
                  305                 310                 315                 320  
  
 Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr  
                  325                 330                 335  
  
 Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val  
                  340                 345                 350  
  
 Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile  
                  355                 360                 365  
  
 Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile  
                  370                 375                 380  
  
 Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala  
                  385                 390                 395                 400  
  
 Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly  
                  405                 410                 415  
  
 Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile  
                  420                 425                 430  
  
 Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala  
                  435                 440                 445  
  
 Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile  
                  450                 455                 460  
  
 Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile  
                  465                 470                 475

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 <211> 1428  
 <212> DNA  
 <213> zea mays

<400> 5  
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 caagctcatg atagtgttct tggaaatcatt ctggggaggtg gtgctgggac tagattgtac         180  
  
 cccttgacaa agaagggtgc caaggctgca gtgccattgg gtgccaacta tagactgatt         240

gatattcctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa	300
ttaactctg ctccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggagg	360
tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac	420
tggtttcagg gtactgcaga tgctgttaagg cagtaattgt ggttgttga ggagcataat	480
tgatggaat ttctaattct tgctggcgat cacctgtacc gcatggacta tgaaaagttc	540
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aaacgtgcaa ctgcattgg cctcatgaaa attgatgaag aagggaggat cattgagtt	660
gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc	720
cttcatgacg tgagggcaaa gaaaaatgcct tatattgcta gcatgggtat ctatgtttc	780
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ggttactggg aagatatcggtt accattgcg gcattttata atgcaaactt gggaaataacc	960
aagaagccaa taccagattt cagttctat gaccgttttgc ctccaaattta tacacaacct	1020
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<210> 6  
 <211> 476  
 <212> PRT  
 <213> zea mays

<400> 6

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala			
1	5	10	15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn		
20	25	30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly

35

40

45

Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile  
65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr  
85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg  
100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu  
115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly  
130 135 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn  
145 150 155 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp  
165 170 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr  
180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu  
195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro  
210 215 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly  
225 230 235 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly  
245 250 255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln  
260 265 270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr  
275 280 285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu  
290 295 300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr  
305 310 315 320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile  
325 330 335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp

340

345

350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys  
355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala  
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu  
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile  
405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg  
420